binding partner interactions, and that such a search will simultaneously identify art related to methods involving measurement of binding as well as dissociation. Thus, it would not impose a serious burden upon the Examiner to search methods measuring binding or dissociation in a single search strategy. Groups I and II should thus be merged for the purposes of examination.

Notwithstanding the lack of a serious burden on the examiner to search methods measuring binding and dissociation as part of a single search strategy, applicants have amended independent claims 1 and 51 to recite the promotion of, or detection of, "binding or dissociation" of the binding partner polypeptides. Applicants have also cancelled claims 14-26, 29, 31, 53 and 54. Applicants submit that the amendments obviate the need for restriction between the groups. More specifically, applicants submit that the measurement of association and dissociation are sufficiently similar with regard to overall methods of measuring polypeptide interaction and modification as not to impose a serious burden upon the Examiner for search purposes.

With regard to the required election of species if either of groups I or II are elected, applicants have elected the group "kinases" with traverse, but applicants submit that phosphatases are sufficiently similar in action as not to impose a serious burden upon the Examiner for examination purposes. Specifically, kinases and phosphatases both influence the phosphorylation status of a substrate. The removal *or* addition of a phosphate can influence the binding or dissociation interaction of a binding pair. That is, the action of a kinase or a phosphatase on a phosphoprotein can influence the binding or dissociation interaction of a binding pair. Therefore, it is logical to consider them in the same group for purposes of examination of the present claims. Applicants request that kinases and phosphatases be considered together without restriction to a single species.

Respectfully submitted,

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Version of amendments marked to show changes:

1. (Amended) A method for monitoring activity of one or more enzymes comprising the steps of:

A. mixing:

(i) one or more tagged binding partner polypeptides;

(ii) one or more binding partner polypeptides that correspond to said one or more tagged binding partner polypeptides of step (i); and

(iii) one or more enzymes that add or remove a moiety to or from said one or more binding partner polypeptides or one or more tagged binding partner polypeptides;

wherein said one or more tagged binding partner polypeptides or said one or more binding partner polypeptides comprise one or more sites for the addition or removal of said moiety, wherein addition or removal of said moiety promotes binding <u>or dissociation</u> of said one or more binding partner polypeptides with the corresponding one or more tagged binding partner polypeptides; under conditions which promote binding <u>or dissociation</u> of said one or more binding partner polypeptides with said one or more tagged binding partners; and

B. detecting said binding <u>or dissociation</u>, wherein detection of binding <u>or dissociation</u> as a result of said mixing is indicative of enzyme activity.

27. (Amended) The method of claim 1 [or 14] wherein said one or more sites comprise a sequence which directs modification by an enzyme selected from the group consisting of a kinase, a phosphatase, a UDP-N-acetylglucosamine-dolichyl-phosphate-N-acetylglucosamine phosphotransferase, an O-GlcNAc transferase, a glycylpeptide-N-tetradecanoyl transferase, a carbohydrate transferase, a ubiquitin activating enzyme El, a ubiquitin conjugating enzyme E2, a ubiquitin conjugating enzyme Ubc9, a ubiquitin protein ligase E3, a poly (ADP-ribose) polymerase, a fatty acyl transferase, and an NAD:Arginine ADP ribosyltransferase.

32. The method of claim 1 [or 14] wherein said tag on said one or more tagged binding partner polypeptides is selected from the group consisting of a coiled-coil, an antigen, an epitope,

an antibody, a single chain antibody, a nucleic acid binding domain, a radioactive amino acid, a fluorescent molecule, a reporter enzyme, and biotin.

33. The method of claim 1 [or 14] wherein said site is recombinant.

34. The method of claim 1 [or 14] wherein said site is naturally occurring.

51. A method of screening for a candidate modulator of enzymatic activity comprising:

A. mixing:

(i) one or more tagged binding partner polypeptides;

(ii) one or more binding partner polypeptides that correspond to said one or more tagged binding partner polypeptides of step (i); and

(iii) one or more enzymes that adds or removes a moiety to or from said binding partner polypeptide or said one or more tagged binding partner polypeptides;

wherein said one or more tagged binding partner polypeptides or said one or more binding partner polypeptides comprise one or more sites for the addition or removal of said moiety, wherein addition or removal of said moiety promotes binding <u>or dissociation</u> of said one or more binding partner polypeptides with the corresponding one or more tagged binding partner polypeptides; under conditions which promote binding <u>or dissociation</u> of said one or more binding partner polypeptides and said one or more tagged binding partner polypeptides; and

B. detecting binding <u>or dissociation</u> of said one or more binding partner polypeptides to said one or more tagged binding partner polypeptides in both the presence and absence of a candidate modulator of enzymatic activity, wherein detection of the amount binding <u>or dissociation</u> in the presence of the candidate modulator that is lesser or greater as compared to the amount of binding <u>or dissociation</u> in the absence of the candidate modulator indicates modulation of enzymatic activity by said candidate modulator.